phosphoglyceromuta

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1 MAEPGHSHHLSARVRGRTER......LGRSNHLPPRGLLMDLTQCR 1001
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 D48776
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translation initia flavoprotein [Impo trypsin (EC 3.4.21) probable modificat hypothetical prote probable sugar-bin succinyl-COA synth hypothetical prote succinyl-COA synth high affinity nitr hypothetical prote Ro/SS-A complex, 6 probable dehydroge developmental prot hypothetical prote DNA repair protein hypothetical prote hypothetical prote carbamoyl-phosphat transcription regu hypothetical prote porphyrin biosynth hypothetical prote probable long-chai histidinol dehydro regulator of epide hypothetical prote hypothetical prote penton base protein nucleolar protein high affinity nitr phosphoglyceromuta gpmB protein - Esc probable uroporphy CT580 hypothetical ct580 hypothetical uroporphyrin-III C transmembrane prot succinate dehydrog uroporphyrinogen methylenetetrahydr probable gamma-glu carbamoyl-phosphat ankyrin-repeat pro carotenoid-binding L-alanine dehydrog hypothetical prote probable anion tra microcin C7 self-i 2-dehydro-3-deoxyphospho-2-dehydro-2-dehydro-3-deoxy-2-dehydro-3-deoxyprobable galactosy
2-dehydro-3-deoxy-LysR-family regula hypothetical prote peroxidase (EC 1.1 tubulin alpha-B ch terrichrome transp conserved hypothet stable inheritance 36K parA protein -

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132 HGFASLSA 139

Matches

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Conservative

100.0%; Pred. No. 5; tive 0; Mismatches

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Indels

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Gaps

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Best Local Similarity

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A; Note:
C; Superf
C; Keywor
                                  A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-133 <HIG>
                                                                R;Higashi, Y.; Kakumu, S.; Yoshioka, K.; Wakita, T.; Mizokami, M.; Ohba, K.; Ito, Y.; Virology 197, 659-668, 1993
A;Title: Dynamics of genome change in the E2/NS1 region of hepatitis C virus in vivo. A;Reference number: A48776; MUID:94069940; PMID:8249288
A;Accession: D48776
                                                                                                             polyprotein (E2/NS1 region, HVR1, HVR2) - hepatitis C virus (fragment) C;Species: hepatitis C virus
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Racession: D48776
                 A; Experimental source: subtype III, patient KS A; Note: sequence extracted from NCBI backbone
                                                                                                                                                     D48776
                                                                                                                                                             RESULT 1
Keywords:
       Note: sequence extracted from NCBI bac
Superfamily: hepatitis C virus genome
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T13173
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Query Match

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Score

8

DВ 2:

Length 133;

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A;Molecule type: protein
A;Residues: 31-338 <WRZ>
A;Residues: 31-338 <WRZ>
R;Gazaryan, I.G.; Chubar, T.A.; Ignatenko, O.V.; Mareeva, E.A.; Orlova, M.A.; Kapeliuch,
Biochem. Biophys. Res. Commun. 262, 297-301, 1999
A;Title: Tryptophanless recombinant horseradish peroxidase: Stability and catalytic prop
A;Reference number: PC7025; MUID:99382281; PMID:10448108
                                                                                                                                                                                                                                                                    A;Title: Covalent structure
A;Reference number: A00502;
A;Accession: A00502
                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 31-338 <WEL>
R;Welinder, K.G.
FEBS Lett. 72, 19-23, 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-353 <FUJ> R;Welinder, K.G. Eur. J. Biochem. 96, 483-502, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peroxidase (EC 1.11.1.7) CIA precursor - horseradish C/Species: Armoracia rusticana (horseradish) C;Date: 24-Apr-1944 #sequence revision 12-Apr-1996 #text_change 01-Dec-2000 C;Accession: $00625; $32972; $\overline{A}00502; $PC7025 R;Fujiyama, K.; Takemura, H.; Shibayama, S.; Kobayashi, K.; Choi, J.K.; Shir Bur. J. Biochem. 173, 681-687, 1988
A;Title: Structure of the horseradish peroxidase isozyme C genes.
A;Reference number: $00625; MUID:88225087; $PMID:3371352
                                                           A; Accession: PC7025
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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
Smitle: The complete genome sequence of the hyperthermophilic, sulfate-reducing arche A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: A69536
A;Molecule type: DNA
A;Residues: 31-338 <GAZ>
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              radish peroxidase C.
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8; Conserv
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                                                                                                                                                                                                                                                                                             of the glycoprotein horseradish peroxidase (EC 1.11.1.7). MUID:77068850; PMID:1001465
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C;Reywords: chromoprotein; glycoprotein; heme; iron; metalloprotein; oxidoreductase; pyr F;1-30/Domain: signal sequence #status predicted <SIG>F;1-38/Product: peroxidase C1 #status experimental <MAT>F;31-38/Product: peroxidase C1 #status experimental <MAT>F;31/Modified site: pyrrolidone carboxylic acid (gln) (in mature form) #status experimental ry-1-121,74-79,127-331,207-239/Disulfide bonds: #status experimental ry-1-121,74-79,127-331,207-239/Disulfide bonds: #status experimental ry-1-188,216,228,244,285,98/Binding site: carbohydrate (Asn) (covalent) #status experimental ry-1-188,216,228,244,285,287,230/Binding site: heme iron (His) (axial ligands) #status predicted
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C;Superfamily: peroxidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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A; Residues: 1-353 < INT>
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A,Description: Nucleotide sequence of a new cDNA for peroxidase from Arabidopsis thalian
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                                                                                                                                                                                                                                                                                                                                           peroxidase - Arabidopsis thaliana
N;Alternate names: protein T2J13.40
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                               A;Reference number: Z23023
A;Accession: T46118
A;Status: preliminary
                                                                                                                                                                                                                                                   R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Ssubmitted to the Protein Sequence Database,
                     A;Experimental source: cultivar Columbia; BAC clone T2J13 C;Genetics:
A;Map position: 3
                                                                                                          A; Molecule type: DNA
A; Residues: 1-353 < RIE>
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100.0%; Pred. N
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100.0%; Pred. No. 11;
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                                                                                                                                                                                                                                                                   S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; base, November 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (axial ligands) #status predicted
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A;Introns: 77/3; 141/3; 198/1
A;Note: T2J13.40
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A; Accession: T46119
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                                                                                                                                                                tolb protein precursor (tolB) RP302 - Rickettsia prowazekii (;Speciles: Rickettsia prowazekii C;Speciles: Rickettsia prowazekii C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 C;Accession: A71886 R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F,69/Active site: Arg #status predicted F,73,201/Binding site: heme iron (His) (axial ligands) #status predicted F,75-80/Disulfide bonds: #status predicted
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A; Residues: 1-354 < RIE>
                     A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-443 <AND>
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                                                                                         A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: A71686
                                                                                                                                                                                                                                                                                                                                                      RESULT 7
A;Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14763.1; PID:g386086
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100.0%; Pred. No. 11;
7ative 0; Mismatches
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100.0%; Pred. No. 11.
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hypothetical protein CPj0458 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
                                                                                 RESULT 10
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C;Superfamily:
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A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: E72075
                                                             F86547
                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE001630; GB:AE001363; NID:g4376740; PIDN:AAD18600.1; PID:g43767
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-695 < ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein - Chlamydophila pneumoniae (strain CWL029) (Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (c.pate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain CWL029
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A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazakii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: F97750
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A; Residues: 1-444 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE006914; PIDN:AAL02944.1; PID:g15619474; GSPDB:GN00173
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A;Gene: tolB; RP302
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100.0%; Pred. No.
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100.0%; Pred. No. 13;
tive 0; Mismatches
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                                 A; Experimental source: strain C; Genetics:
                                                                           A; Molecule type: DNA
A; Residues: 1-744 < LYN>
A; Cross-references: EMBI
                                                                                                                                                                                C;Accession: T39841
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, February 1998
               A; Gene: SPDB:SPBC19G7.10c
                                                                                                                                                                                                                                                topisomerase II associated protein pat1 homolog - fission yeast (Schizosaccharomyces pom
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec:1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
A; Map position: 2
                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                 A;Accession: T39841
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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                 A,Gene: CP0294
C,Superfamily: Chlamydia hypothetical protein CPn0462
                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE002191; GB:AE002161; NID:g7189216; PIDN:AAF38151.1; PID:g718922
A;Experimental source: strain AR39, HL cells
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-695 < REA>
                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein CP0294 [imported] - Chlamydophila pneumoniae (strain AR39) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000 C;Accession: F81592
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A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: F86547
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A;Cross-references: GB:BA000008; NID:g8978828; PIDN:BAA98664.1; GSPDB:GN00142
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C;Accession: F86547
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                                                                                                                                                              Query Match
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                                                   868 VSSCVAGI 875
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67 VSSCVAGI 74
                                                                                                       Local Similarity les 8; Conser
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Local Similarity 100.0%; Pred No. 1/,
Conservative 0; Mismatches
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                                                                                                       Conservative
                                                                                                                                 100.0%;
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100.0%; Pred. No.
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                                                                                                                                                DB 2; Length 695;
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EMBL:AL021839; PIDN:CAA17064.1; GSPDB:GN00067; SPDB:SPBC19G7.10c

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R;Mizuuchi, M.; Weisberg, R.A.; Mizuuchi, K.
Nucleic Acids Res. 14, 3813-3825, 1986
A;Title: DNA sequence of the control region of phage D108: the N-terminal amino acid seq A;Reference number: S07370; MUID:86232621; PMID:3012481
A;Accession: S07931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Tolias, P.P.; DuBow, M.S.
EMBO J. 4, 3031-3037, 1985
A;Title: The cloning and characterization of the bacteriophage D108 regulatory DNA-bindi A;Reference number: A24680; MUID:86055744; PMID:2998774
A;Accession: A24680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding protein Ner - phage D108
C;Species: phage D108
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 22-Jun-1999
C;Accession: A24680; S07931
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                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-75 <OLI>
A;Cross-references: EMBL:Z99165; PIDN:CAB54975.1; GSPDB:GN00066; SPDB:SPAC2F3.17c
                                                                                                                                                                                                                                                                                                                                                                                                                                                     small nuclear ribonucleoprotein, F-like - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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C; Keywords: DNA binding
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A; Residues: 1-73 < MIZ>
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A; Residues: 1-73 <TOL>
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                                                                                                                                                                                                                         A; Experimental source: strain 972h-; cosmid c2F3
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A;Accession: T38534
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                                                                                                                                 A; Introns: 29/1; 67/1
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nes 8; Conserv
  237 RGNNVLY 243
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                                                                Local Similarity
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                                                                  0.7%; Score 7; 1
100.0%; Pred. No.
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0; Mismatches
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: G84870
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N;Alternate names: protein F24G16.80
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47805
C;Date: 47805
C;Date: 4780
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A; Residues: 1-91 <STO>
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u. Bacteriol. 171, 6414-6422, 1989
A;Title: Proteus mirabilis urease:
                                                                                                                                                                urease (EC 3.5.1.5) 11K chain - Proteus mirabilis
N;Alternate names: urease gamma chain
C;Species: Proteus mirabilis
C;Date: 03-Mar-1993 #sequence_revision 02-Dec-1994 #text_change 18-Jun-1999
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A;Map position: 3
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A; Accession: T47805
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                                              R;Jones, B.D.; Mobley, H.L.T. J. Bacteriol. 171, 6414-6422,
                                                                                                                                                                                                                                                                                                                                     RESULT 17
B43719
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A; Residues: 1-91 <DAN>
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                                                                                                                                  C;Accession: B43719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.7%; Score 7;
100.0%; Pred. No.
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100.0%; Pred. No. 42;
tive 0; Mismatches
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42;
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C;Complex: tr
C;Function:
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(/Species: 
A; Note: seq
C; Genetics:
                                                                                                                 A;Accession: B47090
A;Status: preliminary
A;Molecule type: nucleic
A;Residues: 1-100 <D10>
                                                                                                                                                                                                                                                                               A;Title: Characterization of a plasmid-enceded urease g
A;Reference number: A47090; MUID:93194816; PMID:8449894
A;Contents: 1440
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B47090
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A; Residues: 1-100 < MOE>
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C;Genetics:
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A;Accession: B43719
A;Molecule type: DNA
A;Residues: 1-100 <JON>
             Cross-references: GB:L03307; NID:g148150; PIDN:AAA24745.1; PID:g148152
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Best Local 9
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ive 0; Mismatches
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C;Accession: C95075
C;Accession: C95075
C;Accession: C95075
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Petron, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D. nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, J.A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus, A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: C95075
                                                                                  C; Superfamily: Arabidopsis thaliana hypothetical protein T22K7.130
                                                                                                                                                                                                                                                                                                                         R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T22K7.130 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apx-2000 #sequence_revision 20-Apr-2000 #text_change 05-May-2000
C;Accession: T47435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-106 < KUR>
A; Cross-references: GB:
                                                                                                                                                                            A; Experimental source: cultivar Columbia; BAC clone T22K7
                                                                                                                                                                                              A;Residues: 1-116 <RIE>
A;Cross-references: EMBL:AL138641
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A; Accession: T47435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: UreA
C;Superfamily: urease 11K chain; urease 11K chain
C;Keywords: hydrolase
F;1-100/Domain: urease 11K chain homology <UI1>
                          Local Similarity
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ce: strain TIGR4
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Pred. No.
                        Pred. No.
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Mismatches
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zberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
                      DB 2;
o. 51;
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redd arrett, R.A.; Raggan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Accession: C90490
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A; Introns: 27/3; 61/3; 91/3
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A;Cross-references: EMBL:Z81122; PIDN:CAB03353.1; GSPDB:GN00022; CESP:T13F2.2
A;Experimental source: clone T13F2
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: C90490
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; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; A; Title: Genome sequence of Halobacterium species NRC-1. A; Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                      hypothetical protein Vng0670h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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                                                                                                                        C;Accession: H84224
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 <KUR>
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                                                                                                                                                                                                                                                                                        RESULT 24
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Best Local
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Local Similarity 100.0%;
hes 7; Conservation
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7; Conserv
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58;
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                                                                                                                      D.W.; Shukla, H.D.;
                                                 Ebhardt,
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                                                 H.; Lowe, T.M.; L:
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R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R., Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  formylmethionine deformylase (EC 3.5.1.31) - Rickettsia conorii (strain Mal C;Species: Rickettsia conorii (C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
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Query Match
Best Local Similarity
The 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein MJ0773 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
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C;Keywords: hydrolase
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A; Residues: 1-175 < KUR>
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R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.B.; Barbe, Science 293, 2093-2098, 2001
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A; Residues: 1-159 < STO>
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                                                                                                  A; Map position: REV694542-694
C; Superfamily: Methanococcus
                                                                                                                                       A;Cross-references: GB:U67522; GB:L77117; NID:g2826315; PIDN:AAB98777.1; PID:g1499593; C;Genetics:
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                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA_
                                                                                                                                                                                                                                            A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: E64396
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100.0%; Pred. No. 72
ative 0; Mismatches
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100.0%; Pred. No.
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Pred. No.
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                                    DB 2;
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5. 72;
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687 SFTSKGL 693

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R; Parkhill, J.; Wren,
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A;Experimental source: strain R1
C;Genetics:
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A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z67753; NID:g1185127; PIDN:CAA91709.1; PID:g1185226
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
C;Genetics:
                                                                                                       AD0056
                                                                                                                        RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Od
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein 181 - Odontella sinensis chloroplast C;Species: chloroplast Odontella sinensis C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 20-Jun-2000
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Best Local
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Best Local
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       B.W.; Thomson,
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       N.R.; Titball,
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Mismatches
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   R.W.; Holden, M.T.G.; Prentice,
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A;Cross-references: GB:AE005174; NID:g12519424; PIDN:AAG59575.1; GSPDB:GN00145; UWGP:Z5:A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics:
A;Gene: gpmB
                                                                       A; Molecule type: DNA
A; Residues: 1-215 <STO>
                                                                                                                                               A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A; Reference number: A85480; MUID:21074935; PMID:11206551
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phosphoglyceromutase 2 [imported] - Escherichia coli (strain O157:H7, substrain EDL933) c;Species: Escherichia coli (species: Esc
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C;Superfamily: Aquifex aeolicus phosphoglycerate mutase; phosphoglycerate mutase homolog
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 27-Nov-2001
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A; Residues: 1-215 <HAY>
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
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A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: ABO001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                C86139
                                                                                                                                                                                                                                                                                                                RESULT 31
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A; Residues: 1-215 < KUR>
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K.; Whitehead, S.; Barr
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Barrell,
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C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999 (C;Accession: C71843 R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; I'ves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999 A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                     A; Variety: strain J99
C; Date: 12-Feb-1999 #8
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
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N;Alternate names: hypothetical protein o215b
C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                probable uroporphyrinogen-iii synthase - Helicobacter pylori (strain C;Species: Helicobacter nvlovi
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A; Residues: 1-215 < BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B65255
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A;Cross-references: GB:AE001542; (A;Experimental source: strain J99
                                                    A; Molecule type: DNA
A; Residues: 1-223 <ARN>
                                                                                                            A;Status: preliminary
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A;Experimental source: strain K-12, substrain MG1655
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                                                                                                                                                                                                                                                                                                                                                                                       Species: Helicobacter pylori
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                       Cross-references: GB:AE001542; GB:AE001439;
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100.0%; Pred. No. 85;
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                       NID:g4155739; PIDN:AAD06731.1; PID:g415575
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                    Similarity 100.0%; 7; Conservative (
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RiTomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKerson, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: H64672
                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-226 <WOO>
                                                                                                                                                  A;Gene: SPCC1235.08c
                                                                                                                                                                                                                               A;Cross-references: EMBL:AL031764; PIDN:CAA21112.1; GSPDB:GN00068; SPDB:SPCC1235.08c
                                                                                                                                                                                                                                                                                                                                                      A;Reference number: Z21954
A;Accession: T40882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 4, 393-396, 1997
A/Title: Identification and characterization of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Schizosaccharomyces pombe
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
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                                                                                     C; Superfamily: Schizosaccharomyces pombe transmembrane protein
                                                                                                                       A; Map position:
                                                                                                                                                                                                         A; Experimental source: strain 972h-; cosmid c1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.7%; Score 7; DB 2
100.0%; Pred. No. 88;
ive 0; Mismatches
0.7%; Score 7; DB 2;
100.0%; Pred. No. 88;
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%; Pred. No. 87;
0; Mismatches
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Length 226;

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Gaps

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F;40-82/Domain: ferredoxin [2Fe-2S] homology <FER1>
F;414-226/Domain: ferredoxin [2Fe-4S] homology <FER2>
F;144-226/Domain: ferredoxin 2[4Fe-4S] homology <FER2>
F;61,66,69,81/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted F;151,154,157,218/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted F;161,208,214/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                 A; Map position: 3
A; Introns: 12/2; 36/2
                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-244 <LYN>
A;Residues: 1-244 <LYN>
A;Cross-references: EMBL:AL035075; PIDN:CAA22640.1; GSPDB:GN00068; SPDB:SPCC1919.09
A;Experimental source: strain 972h-; cosmid c1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: Z21979
A; Accession: T41234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Lyne, M.; Harris, D.E.; Murphey, L.D.; Rajandream, M.A.; submitted to the EMBL Data Library, January 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation initiation factor eIF-6 [imported] - fission yeast (Schizosacch C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       문
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: fumarate reductase iron-sulfur protein; ferredoxin 2[4Fe-4S] homology; fe C;Keywords: 2Fe-2S; 3Fe-4S; 4Fe-4S; iron-sulfur protein; metalloprotein; mitochondrion; F;40-82/Domain: ferredoxin [2Fe-2S] homology <FERl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Genome: mitochondrion C; Superfamily: fumarate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AF007261; NID:g2258325; PIDN:AAD11913.1; PID:g2258379
A;Experimental source: ATCC 50394
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Lang, B.F.; Burger, G.; O'Kelly, C.J.; Cedergren, R.; Golding, G.B.; L Nature 387, 493-497, 1997
A;Title: An ancestral mitochondrial DNA resembling a eubacterial genome A;Reference number: S78127; MUID:97311393; PMID:9168110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 C;Accession: S78180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             succinate dehydrogenase (ubiquinone) (EC 1.3.5.1) chain 2 - Reclinomonas americana (ATCC N;Alternate names: succinate:ubiquinone oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                         Genetics:
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                            SLPDPVK 93
                                                                            SLPDPVK 87
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                                                                                                                          Similarity 7; Conserv
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                                                                                                                                                                                                                     hypothetical protein YPR016c
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100.0%; Pred. No.
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D. 94;
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c;Superfamily: trypsin; trypsin homology C;Keywords: hydrolase; protein digestion; serine proteinase F;42-261/Domain: trypsin homology <TRY> F;62,127,222/Active site. ""
                                                                                         R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing end A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                       probable modification methylase protein [imported] - Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: H96009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trypsin (EC 3.4.21.4) precursor - African malaria mosquito C;Species: Anopheles gambiae (African malaria mosquito) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_cl
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R;Modara, C.; Bardischewsky, F.; Friedrich, C.G.
U. Bacteriol. 179, 5014-5023, 1997
A;Title: Cloning and characterization of sulfite dehydrogenase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Paracoccus denitrificans
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
C;Accession: T46968
  A; Molecule type: DNA
A; Residues: 1-275 < K
                                               A; Status: preliminary
                                                                       A; Accession: H96009
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A; Residues: 1-267 < MUE>
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submitted to the EMBL Data
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A;Residues: 1-247 <WOD>
A;Cross-references: EMBL:X79242; NID:g2253074; PIDN:CAA55826.1;
A;Experimental source: strain GB17
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Best Local (
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Pred. N
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Pred. No.
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95;
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GB:AL591985; PIDN:CAC49744.1; PID:g15141231; GSPDB:GN00167

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A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                          CiSpecies: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 f.plate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 c;Accession: AF2179 r. Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Sasamoto, S.; Watanabe, A.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacton, Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; P.; Karp, P.; Romero, P.; Zhang, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: linear chromosome C; Superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Redidue: 1-282 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL45317.1; PID:g17743007; GSPDB:GN00187
A:Cross-references: Strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Atu4523 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                  hypothetical protein all2989 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
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A;Reference number: AB2577; PMID:11743193
A;Accession: AG3112
A; Residues: 1-282 < KUR>
                       A; Molecule type: DNA
                                                    A;Status: preliminary
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7; Conserv
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o. 1e+02;
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Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tur
A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                           M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Y
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: A71065
                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable sugar-binding transport system permease protein - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: linear chromosome C; Superfamily: oligopeptide permease protein oppB
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A;Molecule type: DNA
A;Residues: 1-284 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK88920.1; PID:g15158694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: F98174
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C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001
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A;Experimental source: strain PCC 7120
                                                                                                                                      C; Superfamily: inner membrane protein ugpA
                                                                                                                                                              A; Gene: PH1215
                                                                                                                                                                                                       A; Note: this accession replaces
                                                                                                                                                                                                                            A Cross-references: GB:AP000005; NID:g3236132; PIDN:BAA30315.1; A;Experimental source: strain OT3
                                                                                                                                                                                                                                                                               A; Residues: 1-292 < KAW>
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                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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Best Local :
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826 VPGSLLL 832
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100.0%; Pred. No. 1.
ative 0; Mismatches
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o. 1.1e+02;
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kelz, B.,
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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
                                                                                                  succinyl-CoA synthetase alpha chain (AP001515) (imported] - Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: E97675
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A;Experimental sourc
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyactession. T., Wohldmann, P. submitted to the EMBL Data Library, submitted to the sequence of C. e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 201
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
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A; Introns: 67/2; 116/2; 142/1; 220/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T01C4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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A;Cross-references: GB:AE005673; NID:g13421487; PIDN:AAK22325.1; GSPDB:GN00148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-294 < GRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Cross-references: EMBL:U70858; PIDN:AAB09178.1; GSPDB:GN00023; CESP:T01C4.3;Experimental source: strain Bristol N2; clone T01C4
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Graves, T.; Wohldr
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Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; I.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D. Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella A;Reference number: AD3252; PMID:11756688
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A; Residues: 1-300 < KUR>
A; Cross-references: GB: AE008688; PIDN: AAL43618.1;
A; Cross-references: Strain C58 (Dupont)
A; Experimental source: C; Genetics:
                                     A;Molecule type: DNA
A;Residues: 1-300 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL51321.1; PID:g17982017; GSPDB:GN00190
                                                                                                                  A; Accession: AF3269
A; Status: preliminary
                                                                                                                                                                                                                                                                                                      succinate-CoA ligase (ADP-forming) (EC 6.2.1.5) [imported] - Brucella melitensis C;Species: Brucella melitensis C;Species: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
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C;Accession: AD2900
C;Accession: AD2900
C;Accession: AD2900
C;Accession: AD2900
C;Accession: ACI, Kaul, R.; Monks, Raye, G.; Gillet, W.; Grant, C.; Guenthner, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            succinyl-CoA synthetase alpha chain [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
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A;Accession: E97675
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-300 <KUR>
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                      strain 16M
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100.0%; Pr
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A; Map position: I
C; Superfamily: succinate-CoA ligase (ADI
C; Keywords: acid-thiol ligase; coenzyme
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F91181
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A; Residues: 1-300 < ABO>
A; Residues: L-300 < ABO>
A; Rose; L-300 < ABO>
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                                                                                                                                          C;Accession: F91181
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama,
R;Hayasha, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa,
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R;Abouhamad, W.N.; Manson, M.D.
Mol. Microbiol. 14, 1077-1092, 1994
A;Title: The dipeptide permease of Escherichia coli closely resembles other bacterial transference number: S61431; MUID:95231288; PMID:7536291
A;Accession: S61433
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gasawara, N.; Yasunaga,
gna Res. 8, 11-22, 2001
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C;Superfamily: oligopeptide permease protein oppB
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                          A,Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: F91181
                                                                                                                                                                                                                                                                             dipeptide transport system permease protein 2 ECs4422 [imported] - Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Datc: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
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A; Residues: 1-300 <BLAT>
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A;Molecule type: DNA
A;Restidues: 1-300 <HAY-
A;Cross-references: GB:BA000007; PIDN:BAB37845.1; PID:g13363896; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: B86028
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AI0486
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A;Residues: 1-300 <STO>
A;Cross-references: GB:AE005174; NID:g12518266; PIDN:AAG58686.1; GSPDB:GN00145; UWGP:Z4:
A;Experimental source: strain 0157:H7, substrain EDL933
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C;Superfamily: oligopeptide permease protein oppE
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C;Superfamily: oligopeptide permease protein oppB
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A; Residues: 1-300 < KUR >
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A;Title:
                   R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
                                                         ct580 hypothetical protein - Chlamydophila pneumoniae (strain CWL029) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000 C;Accession: D72031
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R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
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A; Residues: 1-303 <STO>
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A; Authors: Parry,
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A; Residues: 1-300 < PAR>
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A;Accession: AG0983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simm
A;Title: Complete genome sequence of a multiple drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dipeptide transport system permease protein DppC STY4170 [imported] - Salmonella C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence revision 09-Nov-2001 #text change 27-Nov-2001
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                                     Best
                                                         Query Match
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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                        A;Gene:
                                                                                  A; Molecule type: DNA
A; Residues: 1-310 < KUR>
                                                                                                                                                                                                                                                                                                            LysR-family regulatory protein YPO0631 [imported] - Yersinia pestis (strain C;Species: Yersinia pestis C;Pate: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
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Gene 164, 95-100, 1995
A;Title: Sequence of a novel virulence-mediating gene, v
A;Beference number: JC4347; MUID:96060845; PMID:7590330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uroporphyrin-III C-methyltransferase (EC 2.1.1.107) homolog - Vibrio anguillarum N;Alternate names: hypothetical 34.8K protein C;Species: Vibrio anguillarum C;Date: 21-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 05-May-2000 C;Accession: JC4347
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JC4347
                                                         A;Cross-references: GB:AL590842; PIDN:CAC89485.1; PID:g15978721; GSPDB:GN00175
                                                                                                                                                       A; Accession: AB0078
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A; Experimental source: VAN20
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A;Molecule type: DNA
A;Residues: 1-303 <ARN>
A;Cross-references: GB:AE001662; GB:AE001363; NID:g4377118; PIDN:AAD18945.1; PID:g43771
                                                                                                                          A; Status: preliminary
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A;Residues: 1-306 <MIL>
A;Cross-references: GB:
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A;Accession: D72031
A;Status: preliminary
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Matches 7
;Superfamily:
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hypothetical protein HI1364
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utive 0;
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100.0%; Pred. No
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Mismatches
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Local Similarity nes 7; Conserv

100.0%;

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0.7%; Score 7; DB 2;

Pred. No. 1.
; Mismatches

1.1e+02

Indels

<u>.</u>

Gaps

0

Length 310;

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.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
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A;Gene: CAC2635
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A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kawai, S.; Matsumoto, Y.; Kajita, S.; Yamada, K.; Katayama, Y.; Morohoshi, N. Biosci. Biotechnol. Biochem. 57, 131-133, 1930.
A;Title: Nucleotide sequence for the genomic DNA encoding an anionic peroxidase gene A;Reference number: JQ2217; MUID:93169019; PMID:7764045
A;Accession: JQ2217
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C;Superfamily: peroxidase
C;Superfamily: peroxidase
C;Keywords: chromoprotein; glycoprotein; heme; iron; metalloprotein; oxidoreductase
E;1-21/Domain: signal sequence #status predicted <SIG>
E;22-318/Product: peroxidase, anionic #status predicted
E;32-318/Product: peroxidase, anionic #status predicted
E;32-111/Disulfide bonds: #status predicted
E;34,91,166,203,253/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 1-318 < K
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RESULT 61
S01774
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                                                                                                             129 VILAGGP 135
                                                                                                                                                                 680 VTLAGGP 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLSARVR 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-318 <KAW>
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                                                                                                                                                                                                                                               Similarity
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100.0%; Pred. No. 1.2e+02
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100.0%; Pred. No. 1.
tive 0; Mismatches
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b. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F82904
           Matches
                                                      Query Match
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R;Tabuchi, A.; Min, Y.N.; Kim, C.K.; Fan, Y.L.; Womble, D.D.; Rownd, R.H. J., Mol. Biol. 202, 511-525, 1988
A;Title: Genetic organization and nucleotide sequence of the stability locus A;Reference number: S01774; MUID:89011976; PMID:3172224
A;Accession: S01774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stable inheritance 36K protein - plasmid NR1
C;Species: plasmid NR1
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 05-Nov-1999
C;Accession: S01774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36K parA protein - Escherichia coli plasmid R1
C;Species: Escherichia coli
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1993
C;Accession: A24920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Genome: plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X12777; NID:g43001; PIDN:CAA31264.1; PID:g43002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-320 < TAB>
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                                                                                                                                                                                                                                                                                                                                  R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir
                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical UU330 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: F82904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A94691;
A; Accession: A24920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Partitioning of plasmid R1. Structural and functional analysis of the parA locu
A;Reference number: A94691; MUID:87060986; PMID:3023637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Gerdes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Genome:
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                                                                                                                                                                   A;Cross-references: GB:AE002130; GB:AF222894; NID:g6899302; PIDN:AAF30739.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-327 <GLA>
                                                                                                                                                                                                                                                                                       A; Accession: F82904
                                                                                                                                                                                                                                                                                                                A; Reference number: A82870
                                                                                               A; Genetic code:
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Mol. Biol. 190, 269-279, 1986
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100.0%; +1
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100.0%; Pred. No. 1.:
tive 0; Mismatches
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100.0%; Pred. No.
                                0.7%; Score 7; DB 2; Le
L00.0%; Pred. No. 1.2e+02;
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                                                       Length 327;
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Local

Similarity 7; Conserv

Conservative

Mismatches

Indels

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2-dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) (Phe-sensitive) - Escherichia N,Alternate names: phospho-2-dehydro-3-deoxyheptonate aldolase; phospho-2-keto-3-deoxyhectoss: Escherichia coli C;Becies: Escherichia coli C;Dațe: 18-Aug-1982 #sequence_revision 17-Dec-1982 #text_change 03-Jun-2002 C;Accession: A01106; B64811
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position:
C; Superfamilv.
         R; Davies, . W.D.; Davidson, B.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T38977; S55491 R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, May 1995
                                                                                                                                                                          RESULT 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-346 <CO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: Z21821
A;Accession: T38977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable galactosyltransferase (EC 2.4.1.-) SPAC5H10.13c [similarity] - fission yeast C;Species: Schizosaccharomyces pombe C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 65
S55491
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A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: A96997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE001437; PIDN:AAK78764.1; PID:915023675; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues:
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Best Local
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                                                                                                                                                                                                                                              TTFHEAS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary; translated from GB/EMBL/DDBJ
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Pred. No.
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Mismatches
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o. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                      1.2e+02;
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RESULT 68
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A;Gene: STY0801
C;Superfamily:
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Nature 413, 848-852, 2001
A;Authors: Parry, C., Quail, M., Rutherford, K.,
A;Title: Complete genome sequence of a multiple d
                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Parkhill, J.; Dougan, G.; James, A.; Parkhill, J.; Dougan, G.; James, A.; Davis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phospho-2-dehydro-3-deoxyheptonate aldolase (DAHP synthetase) phenylalanine C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                      A; Residues: 1-350 < PAR>
                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                            A; Accession: AG0593
                                                                                                                                                                                                                                                                                                                                A;Reference number: AB0502;
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A;Experimental source: strain K12
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd.A.; Rose, D.J.; Mau, B.; Shao, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B64811
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A;Experimental source: strain K-12, substrain MG1655
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A;Title: The nucleotide sequence of aroG, the gene for 3-deoxy-D-arabinoheptulosonate-7
A;Reference number: A01106; MUID:82274236; PMID:6125934
A;Accession: A01106
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97
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AGEFLDM 103
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7; Conser
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                                                                                                                                                                                                   GB:AL513382; PIDN:CAD05217.1; PID:g16501987; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                         G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Cl
Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.;
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141 AGEFLDM 147

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A;Gene:
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A;Cross-references: GB:BA000007; PIDN:BAB34205.1; PID:g13360241; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome A;Reference number: A99629; MUID:21156231; PMID:11258796
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A;Cross-references: GB:AE005174; NID:g12513683; PIDN:AAG55083.1; GSPDB:GN00145; UWGP:Z0:
A;Experimental source: strain O157:H7, substrain EDL933
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R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
Science 193, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: A97788
A;Status: preliminary
                                                                                                                                                                                                                                         microcin C7 self-immunity protein homolog [imported] - Rickettsia conorii (strain Malish C;Species: Rickettsia conorii C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001 C;Accession: A97788
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A; Molecule type: DNA
A; Residues: 1-360 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: mccF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:U32830; GB:L42023; NID:g1574389; PIDN:AAC23197.1; PID:g1574392; C;Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase C;Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-362 < TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Ve A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800 A;Accession: I64128
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C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                       Nature 409, 1007-1011, 2001
A;Authors: Rutter, Seeger, K.; Simon, S.; Simmonds, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                      R.; Davies, R.M.; Devlin, Keam, M.A.; Rutherford, K.M. Nature 409, 1007-1011, 2001
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                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-371 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Horner, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C;Accession: F87100
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C.Species: Mycobacterium leprae
                                                                                                               C; Superfamily: alanine dehydrogenase; alanine dehydrogenase homology
                                                                                                                                                                                                  A;Cross-references: GB:AL450380; NID:g13093357; PIDN:CAC30483.1; GSPDB:GN00147
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                             Query Match
Best Local
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Local Similarity nes 7; Conserv
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                                100.0%;
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100.0%; Pred. No. 1.3
ive 0; Mismatches
                                0.7%; Score 7; DB 2; Length 371; 100.0%; Pred. No. 1.3e+02;
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t; Pred. No. 1.3
0; Mismatches
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           Mismatches
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hypothetical protein DKFZp564M2423.1 - human
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
                                                               R;Wambutt, R.; Heubner, D
submitted to the Protein
                                     A; Reference number: Z17524
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: A70791
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A;Introns: 66/3; 96/1; 122/2; 167/2; 189/3; 210/3; 313/1 C;Superfamily: Caenorhabditis elegans hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA18002.1; PID:e126454
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-386 < COL>
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A;Reference number: Z19222
A;Accession: T20093
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Dec-2000
C;Accession: T20093
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                                                                                                                           Accession: T12456
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                                                                           Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S
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100.0%; Pred. No.
                                                        Sequence Database, June 1999
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100.0%; Pred. No.
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                             C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                      hypothetical protein SA0507 [imported] - Staphylococcus aureus (strain N315)
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A;Experimental source: strain 9a5c

R;Simpson, A,J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, B.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, H.A.; Athors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nuncs, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.F. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; and Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below A;Accession: C82637
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                                                                                                                                                                                                                                                                        A; Contents: annotation
                                                                                                                                                                                                                                                                                                                          A;Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-389 <SIM>
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Nature 406, 151-157, 2000
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C;Species: Xylella fastidiosa
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A;Status: preliminary
A;Molecule type: mRNA
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A;Experimental source: fetal brain; clone DKFZp564M2423
C;Genetics:
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                                                                  Query Match
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0.7%; Score 7; DB 2; I
100.0%; Pred. No. 1.4e+02
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Pred. No.
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o. 1.4e+02;
                                                 Length 389
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: G89822
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-391 <KUR>
A;Cross-references: GB:BA000018; PID:g13700440; PIDN:BAB41738.1; GSPDB:GN00149
A;Cross-references: GB:BA000018; PID:g13700440; PIDN:BAB41738.1; GSPDB:GN00149
                                                                                                                                                                                                                                                                                                                                                                                A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AI2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice. M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable long-chain fatty acid transport protein fadL [imported] - Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AH0334
                                                                                        C >
                                                                                                                                A; Experimental source: strain C; Genetics:
                                                                                                                                                  A;Cross-references: GB:BA000019; PIDN:BAB74755.1; PID:g17132150; A;Experimental source: strain PCC 7120
                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-431 < KUR>
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C;Superfamily: long-chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-423 <KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genome sequence of Yersinia pestis, the causative agent of plague A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AH0334
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                                                                                                                                                                                                                                    A;Status: preliminary
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                                                                                  Superfamily: histidinol dehydrogenase; histidinol dehydrogenase
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                                                                                                               hisD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dehydrogenase [imported] - Nostoc sp.
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  Similarity 7; Conserv
    Conservative
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100.0%; Pred. No.
                   100.0%;
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100.0%; Pred. No. 1.5e
                   0.7%; Score 7;
100.0%; Pred. No.
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    Mismatches
                 ; DB 2; Ler
No. 1.5e+02;
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                                                                                                                                                                      RESULT 82
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ankyrin-repeat protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C;Accession: JQ1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, submitted to the EMBL Data Library, June 1999
A;Reference number: Z21612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T36706
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C;Keywords: nucleomor
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A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulator of epidermal growth factor receptor [imported] - Guillardia theta nucleomorph C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
                       R; Zhang, H.; Scheirer, D.C.; Fowle, W.H.; Goodman, H.M. Plant Cell 4, 1575-1588, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position:
A;Title: Expression of antisense or sense RNA of an ankyrin repeat-containing gene bloc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: strain
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A;Residues: 1-434 <DOU>
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                                                                                                                                                                                                                                                                                                   679 TVTLAGG 685
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7; Conserv
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Pred. No.
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No. 1.5e+02;
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o. 1.5e+02;
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                                                                                          22-Jun-1999
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F;315-347/Domain: a
F;348-380/Domain: a
F;381-413/Domain: a
F;387-419/Domain: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carotenoid-binding protein cbpA - Synechococcus sp. C;Species: Synechococcus sp. C;Date: 03-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 08-Oct-1999 C;Accession: A44751 K; Sherman, D.M.; Sherman, L.A. R;Reddy, K.J.; Masamoto, K.; Sherman, D.M.; Sherman, L.A. J. Bacteriol. 171, 3486-3493, 1989 A;Title: DNA sequence and regulation of the gene (cbpA) encoding the 42-kil, A;Reference number: A44751; MUID:89255122; PMID:2498292
                                                                                                                                                                                                                                                   tubulin alpha-B chain - Neurospora crassa C;Species: Neurospora crassa C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999 C;Accession: S45051 R;Monnat, J.; Turian, G. submitted to the EMBL Data Library, May 1994 A;Description: Two alpha-cubulin genes of Neurospora crassa encode divergent proteins.
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S45051
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                                                                                                                        C; Superfamily: tubulin-
C; Keywords: microtubule
                                                                                                                                        A;Cross-references: EMBL:X79404; NID:g495132; PIDN:CAA55941.1; PID:g495133 C;Superfamily: tubulin.
                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-451 < MON>
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A; Accession: S45051
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A; Accession: A44751
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C;Superfamily: unassigned ankyrin repeat proteins; ankyrin
C;Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-439 < ZHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;387-419/Domain: ankyrin
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ankyrin repeat <RP3>
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ive 0; Mismatches
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1.5e+02;
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1104
hypothetical protein F52F10.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000 C;Accession: T33787
                                                                             RESULT
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A;Introns: 284/3; 324/3; 363/3; 393/3; 429/3
A;Note: F24016.270
                                                                                                                                                                                                                                                                                                                A;Gene: 1mo0233
C;Superfamily: DNA repair protein sms
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Ar
R;Glaser, P.; Frangeul, L.; Buchaud, E.; Durand,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA repair protein Sms homolog lmo0233 [imported] - Listeria monocytogenes (strain
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A;Cross-references: EMBL:AL138647
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R;D'Angelo, M.; Vezzi, A.; Modesto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F24G16.270 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 28-Jul-2000
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b; Pred. No. 1.6
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0; Mismatches
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No. 1.6e+02;
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Dussurget, O.;
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carbamoyl-phosphate synthase, large chain (EC 6.3.-.) - Methanococcus jannaschii (;Species: Methanococcus jannaschii C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 (;Accession: A64472 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R: Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; reon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Accession: A64300; MUID:96337999; PMID:86880807 A;Accession: A64472 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A64472
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197
        A; Molecule type: DNA
A; Residues: 1-487 <BUL>
A; Cross-references: GB:
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A;Introns: 39/1; 122/2; 203/1; 261/1; 308/2; 355/2; 448/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C25E10.3
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A; Residues: 1-473 <STO>
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A;Gene: CESP:F52F10.2
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A;Experimental source: strain Bristol N2; clone F52F10
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A; Residues: 1-471 <GRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: At2g42400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 782 AELFHLE 788
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GB:U67577; GB:L77117; NID:g1592013; PID:g1592023; TIGR:MJ1378; PID:g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.7%; Score 7; DB 2; Le 100.0%; Pred. No. 1.6e+02;
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100.0%; Pred. No. 1.6e+02;
rative 0; Mismatches 0;
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                                                                                                                                                                                 A; Map position: 4
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A; Residues: 1-508
                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z14466
A; Accession: T01937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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                                                     Matches
                                                                                                      Query Match
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                                                   Best Local Similarity
Matches 7; Conserv
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Matches 7; Conserv
     364 LEGAVKL 370
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Services 7; Conserv
                                                                                                                                                                                                                                                                                       1-508 <ABU>
                                                                                                                                                                                                                                                                                                               DNA
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A; Experimental source: strain C; Genetics:
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-lA; Title: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Accession: AF1130
                                                                                                                                                          A;Cross-references: EMBL:AP096370; NID:g3695372; PID:g3695380
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                 R;Abu-Threideh, J.; Stoneking, T.; Langston, Y.; submitted to the EMBL Data Library, October 1998 A;Description: The sequence of A. thaliana F1104.
                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F1104.7 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Start codon: TTG
C;Superfamily: carbamoyl-phosphate synthase large chain; biotin carboxylase homology
C;Keywords: ligase
F;11-470/Domain: biotin carboxylase homology <BCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:NC_003210; PIDN:CAC98524.1; PID:g16409822; GSPDB:GN00177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription regulator homolog lmo0445 [imported] - Listeria monocytogenes C;Species: Listeria monocytogenes
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A;Map position: FOR1326866-1328329
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      Conservative
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    0; Mismatches
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Pred. No.
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                                              Length 508
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    Indels
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Fsihi, H.
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EGD

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penton base protein - fowl adenovirus 1
N;Alternate names: envelope protein
C;Species: Aviadenovirus gall (fowl adenovirus 1, CELO)
C;Date: 08-May-1995 #sequence_revision 14-Feb-1997 #text_change 26-Aug-1999
C;Accession: S52321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleolar protein - human

(;Species: Homo sapiens (man)

(;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C;Date: 15-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C;Accession: JE0335

R;Ueki, N.; Kondo, M.; Seki, N.; Yano, K.; Oda, T.; Masuho, Y.; Muramatsu, M.

Biochem. Biophys. Res. Commun. 252, 97-1027 1998

Biochem. Biophys. Res. Commun. 252, 97-1027 1998

A;Title: NOLP: Identification of a novel human nucleolar protein and determination of selection of a novel human nucleolar protein and determination of selection of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Akopian, T.A.; Lazareva, S.E.; Tikhomirov, E.E.; Karpov, V.A.; Naroditsky, B.S. submitted to the EMBL Data Library, February 1995
A;Description: Genes for Avian adenovirus CELO pentone base and core polypeptides A;Reference number: S53320
A;Accession: S53321
                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-530 <FIL>
                                                                                                                                                                                                                                                           A;Title: Expression analysis of a high affinity nitrate transporter A;Reference number: Z25479; MUID:99136914; PMID:9951738 A;Accession: T51836
                                                                                                                                                                                                                                                                                                                                                                                                                                                               high affinity nitrate transporter protein 2 AtNRT2-1 [similarity] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000 C;Accession: T51836
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A; Residues: 1-524 <UEK>
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C;Superfamily: adenovirus penton protein
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A; Residues: 1-515 < AKO>
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                                                                                           A;Cross-references: EMBL:AF093754; PIDN:AAC64170.1
                                                                                                                                                                                                                                                                                                                                                                                 R; Filleur, S.; Daniel-Vedele, F. Planta 207, 461-469, 1999
                                                        Experimental source: cultivar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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nes 7; Conserv
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A;Map position: 1q31-1q31
C;Keywords: DNA binding; zinc finger
F;305-323/Region: zinc finger CCHH motif
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Ro/SS-A complex, 60K ribonucleoprotein - human ()Species: Homo sapiens (man) ()Species: Homo sapiens (man) ()CjDate: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Oct-1999 ()Accession: A31760; A30596 R;Deutscher, S.L.; Harley, J.B.; Keene, J.D. Proc. Natl. Acad. Sci. U.S.A. 85, 9479-9483, 1988 A;Title: Molecular analysis of the 60-kDa human Ro ribonucleoprotein. A;Reference number: A31760; MUID:89071722; PMID:3200833 A;Accession: A31760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: B89771
                                                                                       A;Molecule type: mRNA
A;Residues: 1-238,'R',240-292,'DV',295-300,'A',302-514,'ALQNTLLNKSF' <BEN>
A;Cross-references: GB:M25077; NID:g387656
A;Note: the sequence is revised in GenBank entry HUMANTARNP, release 111.0,
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C; Keywords: nitrate transport
                                                                                                                                                                                                                          J. Clin. Invest. 83, 1284-1292, 1989
A;Title: Isolation and characterization of a cDNA clone encoding the 60-kD component of
A;Reference number: A30596; MUID:89198084; PMID:2649513
                                                                                                                                                                                                                                                                                                                         A;Residues: 1-538 <DEU>
A;Rosidues: 1-538 <DEU>
A;Cross-references: GB:J04137; NID:g177782; PIDN:AAA35493.1; PID:g177783
R;Ben-Chetrit, B.; Gandy, B.J.; Tan, E.M.; Sullivan, K.F.
J. Clin. Invest. 83, 1284-1292, 1989
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A; Residues: 1-530 < KUR>
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C;Superfamily: nitrate transporter component
A;Cross-references: GDB:355563; OMIM:600063
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Pred. No.
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methylenetetrahydrofolate reductase 2 - fission yeast (Schizosaccharomyces pombe) (Species: Schizosaccharomyces pombe) (Species: Schizosaccharomyces) (Species: Species: 
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A30098
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A;Reference number: A30098; MUID:89252831; PMID:2721962
A;Accession: A30098
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C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 16-Feb-1997
C;Accession: A30098
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A;Experimental source: strain A3(2)
C;Genetics:
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A;Reference number: 221612
A;Recession: T36704
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T36704
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Keywords: DNA binding
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A; Residues: 1-591 <MIL>
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A; Residues: 1-563 < MUR>
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A;Residues: 1-603 <PEA>
A;Cross-references: EMBL:Z69728; PIDN:CAA93581.1; GSPDB:GN00066; SPDB:SPAC56F8.10
A;Experimental source: strain 972h-; cosmid c56F8
C;Genetics:
A;Gene: SPDB:SPAC56F8.10
                                                                                                                                                                                                                                                                                                                                                                                                             R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997
A;Reference number: Z21813
A;Accession: T38908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable gamma-glutamyltransferase (EC 2.3.2.2) SPAC56E4.06c, precursor {similarity} -
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C;Accession: T38908
Search completed: April 22, 2003, 15:36:05
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                                                                                                                                                                                                                          C;Superfamily: gamma-glutamyltransferase
C;Keywords: aminoacyltransferase
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                                                                                                                                                                                                                                                                                    A;Gene:
                                                                                                                                                                                                                                                                                                              A;Residues: 1-611 <CON>
A;Residues: 1-611 <CON>
A;Cross-references: EMBL:Z99261; PIDN:CAB16397.1; GSPDB:GN00066; SPDB:SPAC56E4.06c
A;Experimental source: strain 972h-; cosmid c56E4
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Matches
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                                                                                                                                                                                       Query Match
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                                                                        555 ESGFSKS 561
                                                                                                             727 ESGFSKS 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 WDELPHG 348
                                                                                                                                            Local Similarity
les 7; Conserv
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Pred. No.
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o. 2e+02;
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